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6297.1CP.ST25.txt
SEQUENCE LISTING

<110> Lowery, David E.
Smith, Valdin G.
Kubiak, Teresa M.
Larsen, Martha J.

<120> Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods Related To The Same

<130> 6297.1cp

<140> 09/693,746

<141> 2000-10-20

<150> 09/425,676

<151> 1999-10-22

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<170> PatentIn version 3.1

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20          25          30

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35          40          45

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Asp Glu Asp Arg Ser Gly Gly Ile Ile His Asn Gln Phe Val Gln Ile
50          55          60

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Phe Phe Tyr Val Leu Tyr Ala Thr Val Phe Val Leu Gly Val Phe Gly
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Asn Val Leu Val Cys Tyr Val Val Leu Arg Asn Arg Ala Met Gln Thr
85          90          95

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Val Thr Asn Ile Phe Ile Thr Asn Leu Ala Leu Ser Asp Ile Leu Leu
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Thr Cys Ile Gly Ile Ile Val Ser Ile Trp Val Ile Ala Leu Leu Ala
 180 185 190

Thr Val Pro Tyr Gly Met Tyr Met Lys Met Thr Asn Glu Leu Val Asn
 195 200 205

Gly Thr Gln Thr Gly Asn Glu Thr Leu Val Glu Ala Thr Leu Met Leu
 210 215 220

Asn Gly Ser Phe Val Ala Gln Gly Ser Gly Phe Ile Glu Ala Pro Asp
 225 230 235 240

Ser Thr Ser Ala Thr Gln Ala Tyr Met Gln Val Met Thr Ala Gly Ser
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Thr Gly Pro Glu Met Pro Tyr Val Arg Val Tyr Cys Glu Glu Asn Trp
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Pro Ser Glu Gln Tyr Arg Lys Val Phe Gly Ala Ile Thr Thr Thr Leu
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Asn Val Val Asn Ile Phe Asp Asp Phe Asp Asp Lys Ser Asn Glu Trp
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Arg Phe Tyr Ile Leu Phe Phe Phe Val Ala His Ser Ile Ala Met Ser
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Ser Thr Cys Tyr Asn Pro Phe Leu Tyr Ala Trp Leu Asn Glu Asn Phe
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Arg Lys Glu Phe Lys His Val Leu Pro Cys Phe Asn Pro Ser Asn Asn
 405 410 415

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 420 425 430

Cys Gly Pro Arg Leu His His Gly Lys Gly Asp Gly Gly Met Gly Gly
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Gly Ser Leu Asp Ala Asp Asp Gln Asp Glu Asn Gly Ile Thr Gln Glu
 450 455 460

Thr Cys Leu Pro Lys Glu Lys Leu Leu Ile Ile Pro Arg Glu Pro Thr
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Tyr Gly Asn Gly Thr Gly Ala Val Ser Pro Ile Leu Ser Gly Arg Gly
 485 490 495

Ile Asn Ala Ala Leu Val His Gly Gly Asp His Gln Met His Gln Leu
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Gln Pro Ser His His Gln Gln Val Glu Leu Thr Arg Arg Ile Arg Arg
 515 520 525

Arg Thr Asp Glu Thr Asp Gly Asp Tyr Leu Asp Ser Gly Asp Glu Gln
 530 535 540

Thr Val Glu Val Arg Phe Ser Glu Thr Pro Phe Val Ser Thr Asp Asn
 545 550 555 560

Thr Thr Gly Ile Ser Ile Leu Glu Thr Ser Thr Ser His Cys Gln Asp
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Ser Asp Val Met Val Glu Leu Gly Glu Ala Ile Gly Ala Gly Gly Gly
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Ala Glu Leu Gly Arg Arg Ile Asn
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Ile Asn Gly Thr Leu Pro Trp Ile Val Gly Phe Phe Phe Gly Val Ile
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Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val
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Ala Ala Ala Asp Leu Met Phe Val Ile Leu Cys Ile Pro Phe Thr Ala
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Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg
100 105 110

Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr
115 120 125

Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile
130 135 140

Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val
145 150 155 160

Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr
165 170 175

His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
180 185 190

Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
195 200 205

Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
210 215 220

Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
225 230 235 240

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
245 250 255

Leu Val Val Val Val Val Ile Ala Phe Ala Ser Leu Trp Leu Pro Val
260 265 270

Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
275 280 285

Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
290 295 300

Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe

305 310 315 320

Arg Lys Ala Phe Tyr Lys Ala Val Asn Cys Ser Ser Arg Tyr Gln Asn
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Ser Thr Thr Gly Leu
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 35 40 45

Ala Ile Asn Thr Ser Asp Leu Asn Glu Thr Gly Ser Arg Pro Leu Asp
 50 55 60

Pro Val Leu Ile Asp Arg Phe Leu Ser Asn Arg Ala Val Asp Ser Pro
 65 70 75 80

Trp Tyr His Met Leu Ile Ser Met Tyr Gly Val Leu Ile Val Phe Gly
 85 90 95

Ala Leu Gly Asn Thr Leu Val Val Ile Ala Val Ile Arg Lys Pro Ile
 100 105 110

Met Arg Thr Ala Arg Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp
 115 120 125

Leu Leu Leu Cys Leu Val Thr Met Pro Leu Thr Leu Met Glu Ile Leu
 130 135 140

Ser Lys Tyr Trp Pro Tyr Gly Ser Cys Ser Ile Leu Cys Lys Thr Ile
 145 150 155 160

Ala Met Leu Gln Ala Leu Cys Ile Phe Val Ser Thr Ile Ser Ile Thr
 165 170 175

Ala Ile Ala Phe Asp Arg Tyr Gln Val Ile Val Tyr Pro Thr Arg Asp
 180 185 190

Ser Leu Gln Phe Val Gly Ala Val Thr Ile Leu Ala Gly Ile Trp Ala
 195 200 205

Leu Ala Leu Leu Leu Ala Ser Pro Leu Phe Val Tyr Lys Glu Leu Ile
 210 215 220

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Asn Thr Asp Thr Pro Ala Leu Leu Gln Gln Ile Gly Leu Gln Asp Thr
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Ile Pro Tyr Cys Ile Glu Asp Trp Pro Ser Arg Asn Gly Arg Phe Tyr
 245 250 255

Tyr Ser Ile Phe Ser Leu Cys Val Gln Tyr Leu Val Pro Ile Leu Ile
 260 265 270

Val Ser Val Ala Tyr Phe Gly Ile Tyr Asn Lys Leu Lys Ser Arg Ile
 275 280 285

Thr Val Val Ala Val Gln Ala Ser Ser Ala Gln Arg Lys Val Glu Arg
 290 295 300

Gly Arg Arg Met Lys Arg Thr Asn Cys Leu Leu Ile Ser Ile Ala Ile
 305 310 315 320

Ile Phe Gly Val Ser Trp Leu Pro Leu Asn Phe Phe Asn Leu Tyr Ala
 325 330 335

Asp Met Glu Arg Ser Pro Val Thr Gln Ser Met Leu Val Arg Tyr Ala
 340 345 350

Ile Cys His Met Ile Gly Met Ser Ser Ala Cys Ser Asn Pro Leu Leu
 355 360 365

Tyr Gly Trp Leu Asn Asp Asn Phe Arg Cys Asn Val Gln Ala Ala Ala
 370 375 380

Arg Lys Arg Arg Lys Leu Gly Ala Glu Leu Ser Lys Gly Glu Leu Lys
 385 390 395 400

Leu Leu Gly Pro Gly Gly Ala Gln Ser Gly Thr Ala Gly Gly Glu Gly
 405 410 415

Gly Leu Ala Ala Thr Asp Phe Met Thr Gly His His Glu Gly Gly Leu
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Pro Ser Glu Val Thr Lys Leu Met Pro Arg
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<210> 8
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<212> PRT
<213> D. melanogaster

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<400> 8

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Asn Glu Glu Asn Ile Thr Ser Phe Phe Thr Asp Glu Glu Trp Leu Ala
20           25           30

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Ile Asn Gly Thr Leu Pro Trp Ile Val Gly Phe Phe Phe Gly Val Ile
35           40           45

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Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val
50           55           60

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Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu
65           70           75           80

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6297.1CP.ST25.txt

Ala Ala Ala Asp Leu Met Phe Val Ile Leu Cys Ile Pro Phe Thr Ala
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 100 105 110
 Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr
 115 120 125
 Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile
 130 135 140
 Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val
 145 150 155 160
 Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr
 165 170 175
 His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
 180 185 190
 Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
 195 200 205
 Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
 210 215 220
 Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
 225 230 235 240
 Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
 245 250 255
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 Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
 275 280 285
 Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
 290 295 300
 Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe
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Ser Thr Thr Gly Leu
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 <212> PRT
 <213> D. melanogaster

<400> 10

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Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro Leu Pro Asp
 35 40 45

Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn His Ser Gln
 50 55 60

Thr Leu Ser Thr Asp Gln Pro Ala Val Gly Asp Val Glu Asp Ala Ala
 65 70 75 80

Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala Phe Val Val
 85 90 95

Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly Gly Met Val
 100 105 110

Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile Val Met Thr
 115 120 125

Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ser
 130 135 140

Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe Asn Tyr Tyr
 145 150 155 160

Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr Cys Lys Leu
 165 170 175

Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val Phe Thr Leu
 180 185 190

Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg Pro Leu Gln
 195 200 205

Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala Val Ile Trp
 210 215 220

6297.1CP.ST25.txt

Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile Tyr Arg Thr
 225 230 235 240

Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val Cys Tyr Pro
 245 250 255

Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu Ser Leu Tyr
 260 265 270

Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile Val Ser Met
 275 280 285

Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly Ser Lys Thr
 290 295 300

Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg Ser Lys Arg
 305 310 315 320

Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe Ala Ile Cys
 325 330 335

Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys Tyr Pro Ala
 340 345 350

Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala Ile Tyr Trp
 355 360 365

Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr Cys Trp Met
 370 375 380

Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg Trp Cys Leu
 385 390 395 400

Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu Asn Leu Thr
 405 410 415

Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg Ile Lys Arg
 420 425 430

Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser Ser Pro Lys
 435 440 445

Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala Thr Leu Arg
 450 455 460

Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser Gly Gly Gly
 465 470 475 480

Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln Gln Arg Trp

485

6297.1CP.ST25.txt
490

495

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Asn Thr Thr Gln Leu Leu Ser
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<212> DNA
<213> D. melanogaster

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 ctctcctg 1568

<210> 12
 <211> 522
 <212> PRT
 <213> D. melanogaster

<400> 12

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Leu Phe Ser Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro
 35 40 45

Leu Pro Asp Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn
 50 55 60

His Ser Gln Thr Leu Ser Thr Asp Leu Pro Ala Val Gly Asp Val Glu
 65 70 75 80

Asp Ala Ala Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala
 85 90 95

Phe Val Val Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly
 100 105 110

Gly Met Val Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile
 115 120 125

Val Met Thr Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val
 130 135 140

Asn Leu Ser Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe
 145 150 155 160

Asn Tyr Tyr Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr
 165 170 175

Cys Lys Leu Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val
 180 185 190

Phe Thr Leu Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg
 195 200 205

6297.1CP.ST25.txt

Pro Leu Gln Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala
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 Val Ile Trp Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile
 225 230 235 240
 Tyr Arg Thr Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val
 245 250 255
 Cys Tyr Pro Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu
 260 265 270
 Ser Leu Tyr Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile
 275 280 285
 Val Ser Met Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly
 290 295 300
 Ser Lys Thr Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg
 305 310 315 320
 Ser Lys Arg Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe
 325 330 335
 Ala Ile Cys Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys
 340 345 350
 Tyr Pro Ala Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala
 355 360 365
 Ile Tyr Trp Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr
 370 375 380
 Cys Trp Met Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg
 385 390 395 400
 Trp Cys Leu Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu
 405 410 415
 Asn Leu Thr Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg
 420 425 430
 Ile Lys Arg Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser
 435 440 445
 Ser Pro Lys Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala
 450 455 460

6297.1CP.ST25.txt

Thr Leu Arg Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln
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 500 505 510

Ser Thr Ala Asn Thr Thr Gln Leu Leu Ser
 515 520

<210> 13
 <211> 1394
 <212> DNA
 <213> D. melanogaster

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 aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatc 240
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 agtgcctact ttaagatcat cgtctacatg ctctacattc ccatctttat cttcgccctg 360
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gctcgtcgaa agccacgagc gacatctttg cgagcgaacc cattatcatg cggcgagacg 1380
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<210> 14
 <211> 464
 <212> PRT
 <213> D. melanogaster

<400> 14

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 20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
 35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr
 50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile
 65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu
 85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
 100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
 115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
 130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
 145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu
 165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
 180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
 195 200 205

6297.1CP.ST25.txt

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile
 210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
 225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
 245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr
 260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
 275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
 290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
 305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe
 325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp
 340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
 355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
 370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
 385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
 405 410 415

Met Asn Ala Thr Ser Gly Thr Gly Pro Ala Leu Pro Leu Asn Arg Met
 420 425 430

Asn Thr Ser Thr Thr Tyr Ile Ser Ala Arg Arg Lys Pro Arg Ala Thr
 435 440 445

Ser Leu Arg Ala Asn Pro Leu Ser Cys Gly Glu Thr Ser Pro Leu Arg
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<210> 15

<211> 1556

<212> DNA

<213> D. melanogaster

<400> 15

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<211> 518

<212> PRT

<213> D. melanogaster

<400> 16

6297.1CP.ST25.txt

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20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr
50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu
165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile
210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr

260

265

270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
 275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
 290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
 305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe
 325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp
 340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
 355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
 370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
 385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
 405 410 415

Met Asn Ala Thr Ser Gly Glu Met Thr Thr Lys Tyr His Arg His Val
 420 425 430

Gly Asp Ala Leu Phe Arg Lys Pro Lys Ile Cys Ile Arg Asn Gly Ser
 435 440 445

Ser Thr Ser Ser Gln Ser Asn Glu His Ile His His Leu His Gln Arg
 450 455 460

Ser Ser Lys Ala Thr Ser Asp Ile Phe Ala Ser Glu Pro Ile Ile Met
 465 470 475 480

Arg Arg Asp Val Thr Thr Ala Val Ala Val Ile Ser Lys Asn Lys Thr
 485 490 495

Asp Ser Pro Val Arg Arg Ser Gly Ser Ser Gly Gly Thr Glu Ala Asn
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Ile Arg Ser Thr Glu Phe
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 <211> 1628
 <212> DNA
 <213> D. melanogaster

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 <211> 542
 <212> PRT
 <213> D. melanogaster

<400> 18

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Glu Ile Val Ala Leu Leu Ser Ile Phe Tyr Gly Gly Ile Ser Ile Val
 35 40 45

Ala Val Ile Gly Asn Thr Leu Val Ile Trp Val Val Ala Thr Thr Arg
 50 55 60

Gln Met Arg Thr Val Thr Asn Met Tyr Ile Ala Asn Leu Ala Phe Ala
 65 70 75 80

Asp Val Ile Ile Gly Leu Phe Cys Ile Pro Phe Gln Phe Gln Ala Ala
 85 90 95

Leu Leu Gln Ser Trp Asn Leu Pro Trp Phe Met Cys Ser Phe Cys Pro
 100 105 110

Phe Val Gln Ala Leu Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala
 115 120 125

Ile Ala Ile Asp Arg His Arg Ala Ile Ile Asn Pro Leu Arg Ala Arg
 130 135 140

Pro Thr Lys Phe Val Ser Lys Phe Ile Ile Gly Gly Ile Trp Met Leu
 145 150 155 160

Ala Leu Leu Phe Ala Val Pro Phe Ala Ile Ala Phe Arg Val Glu Glu
 165 170 175

Leu Thr Glu Arg Phe Arg Glu Asn Asn Glu Thr Tyr Asn Val Thr Arg
 180 185 190

Pro Phe Cys Met Asn Lys Asn Leu Ser Asp Asp Gln Leu Gln Ser Phe
 195 200 205

Arg Tyr Thr Leu Val Phe Val Gln Tyr Leu Val Pro Phe Cys Val Ile
 210 215 220

Ser Phe Val Tyr Ile Gln Met Ala Val Arg Leu Trp Gly Thr Arg Ala
 225 230 235 240

Pro Gly Asn Ala Gln Asp Ser Arg Asp Ile Thr Leu Leu Lys Asn Lys
 245 250 255

Lys Lys Val Ile Lys Met Leu Ile Ile Val Val Ile Ile Phe Gly Leu
 260 265 270

Cys Trp Leu Pro Leu Gln Leu Tyr Asn Ile Leu Tyr Val Thr Ile Pro
 275 280 285

Glu Ile Asn Asp Tyr His Phe Ile Ser Ile Val Trp Phe Cys Cys Asp
 290 295 300

Trp Leu Ala Met Ser Asn Ser Cys Tyr Asn Pro Phe Ile Tyr Gly Ile
 305 310 315 320

Tyr Asn Glu Lys Phe Lys Arg Glu Phe Asn Lys Arg Phe Ala Ala Cys
 325 330 335

Phe Cys Lys Phe Lys Thr Ser Met Asp Ala His Glu Arg Thr Phe Ser
 340 345 350

Met His Thr Arg Ala Ser Ser Ile Arg Ser Thr Tyr Ala Asn Ser Ser
 355 360 365

Met Arg Ile Arg Ser Asn Leu Phe Gly Pro Ala Arg Gly Gly Val Asn
 370 375 380

Asn Gly Lys Pro Gly Leu His Met Pro Arg Val His Gly Ser Gly Ala
 385 390 395 400

Asn Ser Gly Ile Tyr Asn Gly Ser Ser Gly Gln Asn Asn Asn Val Asn
 405 410 415

Gly Gln His His Gln His Gln Ser Val Val Thr Phe Ala Ala Thr Pro
 420 425 430

Gly Val Ser Ala Pro Gly Val Gly Val Ala Met Pro Pro Trp Arg Arg
 435 440 445

Asn Asn Phe Lys Pro Leu His Pro Asn Val Ile Glu Cys Glu Asp Asp
 450 455 460

Val Ala Leu Met Glu Leu Pro Ser Thr Thr Pro Pro Ser Glu Glu Leu
 465 470 475 480

Ala Ser Gly Ala Gly Val Gln Leu Ala Leu Leu Ser Arg Glu Ser Ser
 485 490 495

Ser Cys Ile Cys Glu Gln Glu Phe Gly Ser Gln Thr Glu Cys Asp Gly
 500 505 510

Thr Cys Ile Leu Ser Glu Val Ser Arg Val His Leu Pro Gly Ser Gln
 515 520 525

Ala Lys Asp Lys Asp Ala Gly Lys Ser Leu Trp Gln Pro Leu
 530 535 540

<210> 19
 <211> 1451
 <212> DNA
 <213> D. melanogaster

<400> 19
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 aaccatagat ggattagtgg tagttccaca attcagccag aggagtcctt ttatggcact 180
 gatttgccca cctatcaaca ttgcatagcc acgcggaatt cctttgctga cttgttctact 240
 gtggtgctct acggatttgt gtgcattatc ggattatttg gcaacaccct ggtgatctac 300
 gtggtgttgc gcttttccaa aatgcaaacg gtcacgaata tatatattct gaatctggcg 360
 gtggcagacg agtgcttcct gattggaata ccctttctgc tgtacacaat gcgaatttgc 420
 agctggcgat tcggggaggt tatgtgcaaa gcctacatgg tgagcacatc catcacctcc 480
 ttcacctcgt cgatttttct gctcatcatg tccgcggatc gatatatagc ggtatgccac 540
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 gaggatggca tcaattactc gtgcaacata atgtggccag atgcgtacaa gaagcattcg 720
 ggcaccacct tcatactgta cacatttttc ctaggattcg ccacaccgct gtgctttatc 780
 ctgagtttct actacttggg tataaggaaa ctgcgatcgg tgggtcccaa accaggaacg 840
 aagtccaagg agaagaggcg ggctcacagg aaggtcactc gactggtact gacgggtgata 900
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 ctgttgacca gcaatccgca gattcctcca ctgctgccac tgaatgcggg taacaacaat 1260
 tcatcgacca ccacatcctc gaccacgaca gcggaagaaga ccggaaccac ggggacacag 1320
 aaatcatgca attccaatgg caaagtgaca gctccgccgg agaatttgat tatatgtttg 1380

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 acagatttgt a 1451

<210> 20
 <211> 483
 <212> PRT
 <213> D. melanogaster

<400> 20

Met Phe Thr Trp Leu Met Met Asp Val Leu Gln Phe Val Lys Gly Glu
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Met Thr Ala Asp Ser Glu Ala Asn Ala Thr Asn Trp Tyr Asn Thr Asn
 20 25 30

Glu Ser Leu Tyr Thr Thr Glu Leu Asn His Arg Trp Ile Ser Gly Ser
 35 40 45

Ser Thr Ile Gln Pro Glu Glu Ser Leu Tyr Gly Thr Asp Leu Pro Thr
 50 55 60

Tyr Gln His Cys Ile Ala Thr Arg Asn Ser Phe Ala Asp Leu Phe Thr
 65 70 75 80

Val Val Leu Tyr Gly Phe Val Cys Ile Ile Gly Leu Phe Gly Asn Thr
 85 90 95

Leu Val Ile Tyr Val Val Leu Arg Phe Ser Lys Met Gln Thr Val Thr
 100 105 110

Asn Ile Tyr Ile Leu Asn Leu Ala Val Ala Asp Glu Cys Phe Leu Ile
 115 120 125

Gly Ile Pro Phe Leu Leu Tyr Thr Met Arg Ile Cys Ser Trp Arg Phe
 130 135 140

Gly Glu Phe Met Cys Lys Ala Tyr Met Val Ser Thr Ser Ile Thr Ser
 145 150 155 160

Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala Asp Arg Tyr Ile
 165 170 175

Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg Thr Leu His Ile
 180 185 190

Ala Lys Val Val Ser Ala Ile Ala Trp Ser Thr Ser Ala Val Leu Met
 195 200 205

Leu Pro Val Ile Leu Tyr Ala Ser Thr Val Glu Gln Glu Asp Gly Ile

210

215

Asn Tyr Ser Cys Asn Ile Met Trp Pro Asp Ala Tyr Lys Lys His Ser
225 230 235 240

Gly Thr Thr Phe Ile Leu Tyr Thr Phe Phe Leu Gly Phe Ala Thr Pro
245 250 255

Leu Cys Phe Ile Leu Ser Phe Tyr Tyr Leu Val Ile Arg Lys Leu Arg
260 265 270

Ser Val Gly Pro Lys Pro Gly Thr Lys Ser Lys Glu Lys Arg Arg Ala
275 280 285

His Arg Lys Val Thr Arg Leu Val Leu Thr Val Ile Ser Val Tyr Ile
290 295 300

Leu Cys Trp Leu Pro His Trp Ile Ser Gln Val Ala Leu Ile His Ser
305 310 315 320

Asn Pro Ala Gln Arg Asp Leu Ser Arg Leu Glu Ile Leu Ile Phe Leu
325 330 335

Leu Leu Gly Ala Leu Val Tyr Ser Asn Ser Ala Val Asn Pro Ile Leu
340 345 350

Tyr Ala Phe Leu Ser Glu Asn Phe Arg Lys Ser Phe Phe Lys Ala Phe
355 360 365

Thr Cys Met Asn Lys Gln Asp Ile Asn Ala Gln Leu Gln Leu Glu Pro
370 375 380

Ser Val Phe Thr Lys Gln Gly Ser Lys Lys Arg Gly Gly Ser Lys Arg
385 390 395 400

Leu Leu Thr Ser Asn Pro Gln Ile Pro Pro Leu Leu Pro Leu Asn Ala
405 410 415

Gly Asn Asn Asn Ser Ser Thr Thr Thr Ser Ser Thr Thr Thr Ala Glu
420 425 430

Lys Thr Gly Thr Thr Gly Thr Gln Lys Ser Cys Asn Ser Asn Gly Lys
435 440 445

Val Thr Ala Pro Pro Glu Asn Leu Ile Ile Cys Leu Ser Glu Gln Gln
450 455 460

Glu Ala Phe Cys Thr Thr Ala Arg Arg Gly Ser Gly Ala Val Gln Gln
465 470 475 480

Thr Asp Leu

<210> 21
 <211> 1754
 <212> DNA
 <213> D. melanogaster

<400> 21
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 cggatgcgta ccataaccaa cgtgttcctg ctcaacctgg ccatacggga catgctgctg 480
 ggcgtgctct gcatgcccggt caccctgggtg ggcacctgc tgcgaaactt catctttggc 540
 gagttcctct gcaagctctt tcagttctcg caagccgcct ccgtggccgt ttcgtcctgg 600
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 tcctggcaga caatcagtc cgcctacaag atcatcggt tcacttggt gggcggcac 720
 ctctgcatga cgcccatagc ggtctttagt caattgatac ccaccagtcg accgggctac 780
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aacaccaaca ttagtctcaa tcccggccta gccatgggta tgggcacctg gcggagtcgc 1680
 tcacgccacg agtttctcaa tgcggtggtg accaccaata gtgccgccgc cgcggtcaac 1740
 agtcctcagc tcta 1754

<210> 22
 <211> 584
 <212> PRT
 <213> D. melanogaster

<400> 22

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Ala Ala Ala Tyr Arg Ala Leu Leu Asp Tyr Tyr Ala Asn Ala Pro Ser
 20 25 30

Ala Ala Gly His Ile Val Ser Leu Asn Val Ala Pro Tyr Asn Gly Thr
 35 40 45

Gly Asn Gly Gly Thr Val Ser Leu Ala Gly Asn Ala Thr Ser Ser Tyr
 50 55 60

Gly Asp Asp Asp Arg Asp Gly Tyr Met Asp Thr Glu Pro Ser Asp Leu
 65 70 75 80

Val Thr Glu Leu Ala Phe Ser Leu Gly Thr Ser Ser Ser Pro Ser Pro
 85 90 95

Ser Ser Thr Pro Ala Ser Ser Ser Ser Thr Ser Thr Gly Met Pro Val
 100 105 110

Trp Leu Ile Pro Ser Tyr Ser Met Ile Leu Leu Phe Ala Val Leu Gly
 115 120 125

Asn Leu Leu Val Ile Ser Thr Leu Val Gln Asn Arg Arg Met Arg Thr
 130 135 140

Ile Thr Asn Val Phe Leu Leu Asn Leu Ala Ile Ser Asp Met Leu Leu
 145 150 155 160

Gly Val Leu Cys Met Pro Val Thr Leu Val Gly Thr Leu Leu Arg Asn
 165 170 175

Phe Ile Phe Gly Glu Phe Leu Cys Lys Leu Phe Gln Phe Ser Gln Ala
 180 185 190

Ala Ser Val Ala Val Ser Ser Trp Thr Leu Val Ala Ile Ser Cys Glu
 195 200 205

Arg Tyr Tyr Ala Ile Cys His Pro Leu Arg Ser Arg Ser Trp Gln Thr
 210 215 220

Ile Ser His Ala Tyr Lys Ile Ile Gly Phe Ile Trp Leu Gly Gly Ile
 225 230 235 240

Leu Cys Met Thr Pro Ile Ala Val Phe Ser Gln Leu Ile Pro Thr Ser
 245 250 255

Arg Pro Gly Tyr Cys Lys Cys Arg Glu Phe Trp Pro Asp Gln Gly Tyr
 260 265 270

Glu Leu Phe Tyr Asn Ile Leu Leu Asp Phe Leu Leu Leu Val Leu Pro
 275 280 285

Leu Leu Val Leu Cys Val Ala Tyr Ile Leu Ile Thr Arg Thr Leu Tyr
 290 295 300

Val Gly Met Ala Lys Asp Ser Gly Arg Ile Leu Gln Gln Ser Leu Pro
 305 310 315 320

Val Ser Ala Thr Thr Ala Gly Gly Ser Ala Pro Asn Pro Gly Thr Ser
 325 330 335

Ser Ser Ser Asn Cys Ile Leu Val Leu Thr Ala Thr Ala Val Tyr Asn
 340 345 350

Glu Asn Ser Asn Asn Asn Asn Gly Asn Ser Glu Gly Ser Ala Gly Gly
 355 360 365

Gly Ser Thr Asn Met Ala Thr Thr Thr Leu Thr Thr Arg Pro Thr Ala
 370 375 380

Pro Thr Val Ile Thr Thr Thr Thr Thr Thr Val Thr Leu Ala Lys
 385 390 395 400

Thr Ser Ser Pro Ser Ile Arg Val His Asp Ala Ala Leu Arg Arg Ser
 405 410 415

Asn Glu Ala Lys Thr Leu Glu Ser Lys Lys Arg Val Val Lys Met Leu
 420 425 430

Phe Val Leu Val Leu Glu Phe Phe Ile Cys Trp Thr Pro Leu Tyr Val
 435 440 445

Ile Asn Thr Met Val Met Leu Ile Gly Pro Val Val Tyr Glu Tyr Val
 450 455 460

Asp Tyr Thr Ala Ile Ser Phe Leu Gln Leu Leu Ala Tyr Ser Ser Ser
465 470 475 480

Cys Cys Asn Pro Ile Thr Tyr Cys Phe Met Asn Ala Ser Phe Arg Arg
485 490 495

Ala Phe Val Asp Thr Phe Lys Gly Leu Pro Trp Arg Arg Gly Ala Gly
500 505 510

Ala Ser Gly Gly Val Gly Gly Ala Ala Gly Gly Gly Leu Ser Ala Ser
515 520 525

Gln Ala Gly Ala Gly Pro Gly Ala Tyr Ala Ser Ala Asn Thr Asn Ile
530 535 540

Ser Leu Asn Pro Gly Leu Ala Met Gly Met Gly Thr Trp Arg Ser Arg
545 550 555 560

Ser Arg His Glu Phe Leu Asn Ala Val Val Thr Thr Asn Ser Ala Ala
565 570 575

Ala Ala Val Asn Ser Pro Gln Leu
580

<210> 23
<211> 1452
<212> DNA
<213> D. melanogaster

<400> 23
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ggcaacgggg ccaatgacag cggactcctg gcaaccggac aaggtctgga gcaggagcag 120
gagggtcttg cactggatat gggccacaat gccagcgccg acggcggaat agtaccgtat 180
gtgcccgtgc tggaccgccc ggagacgtac attgtcaccg tgctgtacac gtcacatctc 240
attgtgggag ttttgggcaa cggcacgctg gtcacatctt tctttcgcca ccgctccatg 300
cgcaacatac ccaacacata cattctttca ctggccctgg ctgatctgtt gggttatattg 360
gtgtgtgtac ctgtggccac gattgtctac acgcaggaaa gctggccctt tgagcggaac 420
atgtgccgca tcagcgagtt cttaaggac atatccatcg ggggtgtccgt gtttacactg 480
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aagccgctca ctgtctttac tgcggtgatg atctggatcc tggccatcct actgggcatg 600
ccttcggttc ttttctccga catcaagtcc taccctgtgt tcacagccac cggtaacatg 660
accattgaag tgtgtctccc atttcgcgac ccggagtatg caaagttcat ggtggcgggc 720
aaggcactgg tgtactacct gttgccgctg tccatcattg gggcgctata catcatgatg 780

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ttcttcatct gtttcttccc gtaccacgtg tttgagctgt ggtaccactt ctaccaaacg      960
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caaccccggtg gcctctactg cgtgtccggg gtgtttcggc agcactttta tcgctacctc      1080
tgctgcatct gcgtcaagcg gcagccgcac ctgcggcagc actcaacggc cactggaatg      1140
atggacaata ccagtgtgat gtccatgcgc cgctccacgt acgtgggtgg aaccgctggc      1200
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gtaggaggag gagtagggtc aggtcgtgtg ggcagctttc atcggcagga ctcgatgccc      1320
ctgcagcacg gaaatgccca cggaggtggt gcgggcgggg gatcctccgg acttgagacc      1380
ggcgggcgga cggcggcagt gagcgaaaag agctttataa atcgttacga aagtggcgta      1440
atcgctact aa                                                                1452

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<210> 24
<211> 483
<212> PRT
<213> D. melanogaster

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<400> 24
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Met Tyr Ala Ser Leu Met Asp Val Gly Gln Thr Leu Ala Ala Arg Leu
1           5           10           15
```

```
Ala Asp Ser Asp Gly Asn Gly Ala Asn Asp Ser Gly Leu Leu Ala Thr
20           25           30
```

```
Gly Gln Gly Leu Glu Gln Glu Gln Gly Leu Ala Leu Asp Met Gly
35           40           45
```

```
His Asn Ala Ser Ala Asp Gly Gly Ile Val Pro Tyr Val Pro Val Leu
50           55           60
```

```
Asp Arg Pro Glu Thr Tyr Ile Val Thr Val Leu Tyr Thr Leu Ile Phe
65           70           75           80
```

```
Ile Val Gly Val Leu Gly Asn Gly Thr Leu Val Ile Ile Phe Phe Arg
85           90           95
```

```
His Arg Ser Met Arg Asn Ile Pro Asn Thr Tyr Ile Leu Ser Leu Ala
100          105          110
```

```
Leu Ala Asp Leu Leu Val Ile Leu Val Cys Val Pro Val Ala Thr Ile
115          120          125
```

```
Val Tyr Thr Gln Glu Ser Trp Pro Phe Glu Arg Asn Met Cys Arg Ile
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130

135

140

Ser Glu Phe Phe Lys Asp Ile Ser Ile Gly Val Ser Val Phe Thr Leu
 145 150 155 160

Thr Ala Leu Ser Gly Glu Arg Tyr Cys Ala Ile Val Asn Pro Leu Arg
 165 170 175

Lys Leu Gln Thr Lys Pro Leu Thr Val Phe Thr Ala Val Met Ile Trp
 180 185 190

Ile Leu Ala Ile Leu Leu Gly Met Pro Ser Val Leu Phe Ser Asp Ile
 195 200 205

Lys Ser Tyr Pro Val Phe Thr Ala Thr Gly Asn Met Thr Ile Glu Val
 210 215 220

Cys Ser Pro Phe Arg Asp Pro Glu Tyr Ala Lys Phe Met Val Ala Gly
 225 230 235 240

Lys Ala Leu Val Tyr Tyr Leu Leu Pro Leu Ser Ile Ile Gly Ala Leu
 245 250 255

Tyr Ile Met Met Ala Lys Arg Leu His Met Ser Ala Arg Asn Met Pro
 260 265 270

Gly Glu Gln Gln Ser Met Gln Ser Arg Thr Gln Ala Arg Ala Arg Leu
 275 280 285

His Val Ala Arg Met Val Val Ala Phe Val Val Val Phe Phe Ile Cys
 290 295 300

Phe Phe Pro Tyr His Val Phe Glu Leu Trp Tyr His Phe Tyr Pro Thr
 305 310 315 320

Ala Glu Glu Asp Phe Asp Glu Phe Trp Asn Val Leu Arg Ile Leu Pro
 325 330 335

Lys Leu Val Arg Gln Pro Arg Gly Leu Tyr Cys Val Ser Gly Val Phe
 340 345 350

Arg Gln His Phe Asn Arg Tyr Leu Cys Cys Ile Cys Val Lys Arg Gln
 355 360 365

Pro His Leu Arg Gln His Ser Thr Ala Thr Gly Met Met Asp Asn Thr
 370 375 380

Ser Val Met Ser Met Arg Arg Ser Thr Tyr Val Gly Gly Thr Ala Gly
 385 390 395 400

Asn Leu Arg Ala Ser Leu His Arg Asn Ser Asn His Gly Val Gly Gly
 405 410 415

Ala Gly Gly Gly Val Gly Gly Gly Val Gly Ser Gly Arg Val Gly Ser
 420 425 430

Phe His Arg Gln Asp Ser Met Pro Leu Gln His Gly Asn Ala His Gly
 435 440 445

Gly Gly Ala Gly Gly Gly Ser Ser Gly Leu Gly Ala Gly Gly Arg Thr
 450 455 460

Ala Ala Val Ser Glu Lys Ser Phe Ile Asn Arg Tyr Glu Ser Gly Val
 465 470 475 480

Met Arg Tyr

<210> 25
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 25

Thr Asp Val Asp His Val Phe Leu Arg Phe
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<210> 26
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 <212> PRT
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<220>
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<400> 26

Asp Pro Lys Gln Asp Phe Met Arg Phe
 1 5

<210> 27
 <211> 7
 <212> PRT
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<220>
 <223> Novel Sequence

<400> 27

Pro Asp Asn Phe Met Arg Phe

1

5

<210> 28
<211> 9
<212> PRT
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<400> 28

Thr Pro Ala Glu Asp Phe Met Arg Phe
1 5

<210> 29
<211> 9
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<220>
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<400> 29

Ser Leu Lys Gln Asp Phe Met His Phe
1 5

<210> 30
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<223> Novel Sequence

<400> 30

Ser Val Lys Gln Asp Phe Met His Phe
1 5

<210> 31
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 31

Ala Ala Met Asp Arg Tyr
1 5

<210> 32
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 32

Ser Val Gln Asp Asn Phe Met His Phe
1 5

<210> 33

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 33

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe
1 5 10

<210> 34

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 34

Gly Asp Gly Arg Leu Tyr Ala Phe Gly Leu
1 5 10

<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 35

Asp Arg Leu Tyr Ser Phe Gly Leu
1 5

<210> 36

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 36

Ala Pro Ser Gly Ala Gln Arg Leu Tyr Gly Phe Gly Leu
1 5 10

<210> 37

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 37

Gly Gly Ser Leu Tyr Ser Phe Gly Leu
1 5

<210> 38
<211> 4
<212> PRT
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<220>
<223> Novel Sequence

<400> 38

Phe Ile Arg Phe
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<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 39

Lys Asn Glu Phe Ile Arg Phe
1 5

<210> 40
<211> 4
<212> PRT
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<220>
<223> Novel Sequence

<400> 40

Phe Met Arg Phe
1

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 41

Lys Ser Ala Phe Met Arg Phe
1 5

<210> 42
<211> 7
<212> PRT
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<220>
<223> Novel Sequence

<400> 42

Lys Pro Asn Phe Leu Arg Phe
1 5

<210> 43
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 43

Phe Leu Arg Phe
1

<210> 44
<211> 4
<212> PRT
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<220>
<223> Novel Sequence

<400> 44

Tyr Leu Arg Phe
1

<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 45

Lys Pro Asn Phe Leu Arg Tyr
1 5

<210> 46
<211> 8
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<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 46

Thr Asn Arg Asn Phe Leu Arg Phe
1 5

<210> 47

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